

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Presta, Leonard G.
Shelton, David L.
Urfer, Roman

(ii) TITLE OF INVENTION: HUMAN trk RECEPTORS AND NEUROTROPHIC FACTOR INHIBITORS

(iii) NUMBER OF SEQUENCES: 41

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Knobbe, Martens, Olson & Bear, LLP
(B) STREET: 620 Newport Center Drive, 16th Floor
(C) CITY: Newport Beach
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 92660

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: not yet assigned
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/446172
(B) FILING DATE: 19-MAY-1995

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/286846
(B) FILING DATE: 05-AUG-1994

(xi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/215139
(B) FILING DATE: 18-MAR-1994

(x) ATTORNEY/AGENT INFORMATION:

(A) NAME: Dreger, Ginger
(B) REGISTRATION NUMBER: 33,055
(C) REFERENCE/DOCKET NUMBER: GENENT.33CPC4C

(xi) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 954-4114
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0096449960

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3194 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(ii) MOLECULE TYPE: nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAAGGTTTA AAGAAGAAGC CGCAAAGCGC AGGGAAGGCC TCCCGGCACG 50
GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100
CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150
CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200
TTCGCCTGTC CCACGTCCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250
CGACCCTTCT CCTGGCATCG TGGCATTTCC GAGATTGGAG CCTAACAGTG 300
TAGATCCTGA GAACATCACC GAAATTTTCA TCGCAAACCA GAAAAGGTTA 350
GAAATCATCA ACGAAGATGA TGTGAAGCT TATGTGGGAC TGAGAAATCT 400
GACAATTGTG GATTCTGGAT TAAAATTTGT GGCTCATAAA GCATTTCTGA 450
AAAACAGCAA CCTGCAGCAC ATCAATTTTA CCCGAAACAA ACTGACGAGT 500
TTGTCTAGGA AACATTTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550
GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600
AAGAGGCTAA ATCCAGTCCA GACACTCAGG ATTTGTACTG CCTGAATGAA 650
AGCAGCAAGA ATATTCCCCT GGCAAACCTG CAGATACCCA ATTGTGGTTT 700
GCCATCTGCA AATCTGGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750
CTATCACATT ATCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800
TGGGATGTTG GTAACCTGGT TTCAAACAT ATGAATGAAA CAAGCCACAC 850
ACAGGGCTCC TTAAGGATAA CTAACATTTT ATCCGATGAC AGTGGGAAGC 900
AGATCTCTTG TGTGGCGGAA AATCTTGTAG GAGAAGATCA AGATTCTGTC 950
AACCTCACTG TGCATTTTGC ACCAACTATC ACATTTCTCG AATCTCCAAC 1000

CTCAGACCAC CACTGGTGCA TTCCATTAC TGTGAAAGGC AACCCAAAAC 1050
 CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAAATAC 1100
 ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150
 CCAGCTGGAT AATCCCACTC ACATGAACAA TGGGGACTAC ACTCTAATAG 1200
 CCAAGAATGA GTATGGGAAG GATGAGAAAC AGATTTCTGC TCACTTCATG 1250
 GGCTGGCCTG GAATTGACGA TGGTGCAAAC CCAAATTATC CTGATGTAAT 1300
 TTATGAAGAT TATGGAAGT CAGCGAATGA CATCGGGGAC ACCACGAACA 1350
 GAAGTAATGA AATCCCTTCC ACAGACGTCA CTGATAAAAC CGGTCGGGAA 1400
 CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTTG 1450
 CCTTTTGGTA ATGCTGTTTC TGCTTAAGTT GGCAAGACAC TCCAAGTTTG 1500
 GCATGAAAGG CCCAGCCTCC GTTATCAGCA ATGATGATGA CTCTGCCAGC 1550
 CCACTCCATC ACATCTCCAA TGGGAGTAAC ACTCCATCTT CTTCGGAAGG 1600
 TGGCCCAGAT GCTGTCATTA TTGGAATGAC CAAGATCCCT GTCATTGAAA 1650
 ATCCCCAGTA CTTTGGCATC ACCAACAGTC AGCTCAAGCC AGACACATTT 1700
 GTTCAGCACA TCAAGCGACA TAACATTGTT CTGAAAAGGG AGCTAGGCCA 1750
 AGGAGCCTTT GGAAAAGTGT TCCTAGCTGA ATGCTATAAC CTCTGTCCTG 1800
 AGCAGGACAA GATCTTGGTG GCAGTGAAGA CCCTGAAGGA TGCCAGTGAC 1850
 AATGCACGCA AGGACTTCCA CCGTGAGGCC GAGCTCCTGA CCAACCTCCA 1900
 GCATGAGCAC ATCGTCAAGT TCTATGGCGT CTGCGTGGAG GGCACCCCC 1950
 TCATCATGGT CTTTGAGTAC ATGAAGCATG GGGACCTCAA CAAGTTCCTC 2000
 AGGGCACACG GCCCTGATGC CGTGCTGATG GCTGAGGGCA ACCCGCCAC 2050
 GGAAGTACG CAGTCGCAGA TGCTGCATAT AGCCCAGCAG ATCGCCGCGG 2100
 GCATGGTCTA CCTGGCGTCC CAGCACTTCG TGCACCGCGA TTTGGCCACC 2150
 AGGAACTGCC TGGTCGGGGA GAACTTGCTG GTGAAAATCG GGGACTTTGG 2200
 GATGTCCCGG GACGTGTACA GCACTGACTA CTACAGGGTC GGTGGCCACA 2250
 CAATGCTGCC CATTGCTGG ATGCCCTCCAG AGAGCATCAT GTACAGGAAA 2300

TTCACGACGG AAAGCGACGT CTGGAGCCTG GGGGTCGTGT TGTGGGAGAT 2350
 TTTCACCTAT GGCAAACAGC CCTGGTACCA GCTGTCAAAC AATGAGGTGA 2400
 TAGAGTGTAT CACTCAGGGC CGAGTCCTGC AGCGACCCCG CACGTGCCCC 2450
 CAGGAGGTGT ATGAGCTGAT GCTGGGGTGC TGGCAGCGAG AGCCCCACAT 2500
 GAGGAAGAAC ATCAAGGGCA TCCATACCCT CCTTCAGAAC TTGGCCAAGG 2550
 CATCTCCGGT CTACCTGGAC ATTCTAGGCT AGGGCCCTTT TCCCCAGACC 2600
 GATCCTTCCC AACGTACTCC TCAGACGGGC TGAGAGGATG AACATCTTTT 2650
 AACTGCCGCT GGAGGCCACC AAGCTGCTCT CCTTCACTCT GACAGTATTA 2700
 ACATCAAAGA CTCCGAGAAG CTCTCGAGGG AAGCAGTGTG TACTTCTTCA 2750
 TCCATAGACA CAGTATTGAC TTCTTTTTTG CATTATCTCT TTCTCTCTTT 2800
 CCATCTCCCT TGGTTGTTCC TTTTCTTTT TTTAAATTTT CTTTTTCTTC 2850
 TTTTTTTTCG TCTTCCCTGC TTCACGATTC TTACCCTTTC TTTTGAATCA 2900
 ATCTGGCTTC TGCATTACTA TTAActCTGC ATAGACAAAG GCCTTAACAA 2950
 ACGTAATTTG TTATATCAGC AGACACTCCA GTTTGCCCAC CACAACTAAC 3000
 AATGCCTTGT TGTATTCCTG CCTTTGATGT GGATGAAAAA AAGGGAAAAAC 3050
 AAATATTTCA CTAAACTTT GTCActTCTG CTGTACAGAT ATCGAGAGTT 3100
 TCTATGGATT CACTTCTATT TATTTATTAT TATTACTGTT CTTATTGTTT 3150
 TTGGATGGCT TAAGCCTGTG TATAAAAAAA AAAAAAATC TAGA 3194

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 822 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Ser	Trp	Ile	Arg	Trp	His	Gly	Pro	Ala	Met	Ala	Arg	Leu
1				5					10					15
Trp	Gly	Phe	Cys	Trp	Leu	Val	Val	Gly	Phe	Trp	Arg	Ala	Ala	Phe
				20					25					30

Ala	Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ala	Ser	Arg	Ile	Trp	Cys	
				35					40					45	
Ser	Asp	Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro	
				50					55					60	
Asn	Ser	Val	Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Phe	Ile	Ala	Asn	
				65					70					75	
Gln	Lys	Arg	Leu	Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr	
				80					85					90	
Val	Gly	Leu	Arg	Asn	Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe	
				95					100					105	
Val	Ala	His	Lys	Ala	Phe	Leu	Lys	Asn	Ser	Asn	Leu	Gln	His	Ile	
				110					115					120	
Asn	Phe	Thr	Arg	Asn	Lys	Leu	Thr	Ser	Leu	Ser	Arg	Lys	His	Phe	
				125					130					135	
Arg	His	Leu	Asp	Leu	Ser	Glu	Leu	Ile	Leu	Val	Gly	Asn	Pro	Phe	
				140					145					150	
Thr	Cys	Ser	Cys	Asp	Ile	Met	Trp	Ile	Lys	Thr	Leu	Gln	Glu	Ala	
				155					160					165	
Lys	Ser	Ser	Pro	Asp	Thr	Gln	Asp	Leu	Tyr	Cys	Leu	Asn	Glu	Ser	
				170					175					180	
Ser	Lys	Asn	Ile	Pro	Leu	Ala	Asn	Leu	Gln	Ile	Pro	Asn	Cys	Gly	
				185					190					195	
Leu	Pro	Ser	Ala	Asn	Leu	Ala	Ala	Pro	Asn	Leu	Thr	Val	Glu	Glu	
				200					205					210	
Gly	Lys	Ser	Ile	Thr	Leu	Ser	Cys	Ser	Val	Ala	Gly	Asp	Pro	Val	
				215					220					225	
Pro	Asn	Met	Tyr	Trp	Asp	Val	Gly	Asn	Leu	Val	Ser	Lys	His	Met	
				230					235					240	
Asn	Glu	Thr	Ser	His	Thr	Gln	Gly	Ser	Leu	Arg	Ile	Thr	Asn	Ile	
				245					250					255	
Ser	Ser	Asp	Asp	Ser	Gly	Lys	Gln	Ile	Ser	Cys	Val	Ala	Glu	Asn	
				260					265					270	
Leu	Val	Gly	Glu	Asp	Gln	Asp	Ser	Val	Asn	Leu	Thr	Val	His	Phe	
				275					280					285	
Ala	Pro	Thr	Ile	Thr	Phe	Leu	Glu	Ser	Pro	Thr	Ser	Asp	His	His	

	290		295		300
Trp Cys Ile Pro	Phe Thr Val Lys Gly	Asn Pro Lys Pro	Ala Leu		
	305		310		315
Gln Trp Phe Tyr	Asn Gly Ala Ile Leu	Asn Glu Ser Lys Tyr	Ile		
	320		325		330
Cys Thr Lys Ile	His Val Thr Asn His	Thr Glu Tyr His Gly	Cys		
	335		340		345
Leu Gln Leu Asp	Asn Pro Thr His Met	Asn Asn Gly Asp Tyr	Thr		
	350		355		360
Leu Ile Ala Lys	Asn Glu Tyr Gly Lys	Asp Glu Lys Gln Ile	Ser		
	365		370		375
Ala His Phe Met	Gly Trp Pro Gly Ile	Asp Asp Gly Ala Asn	Pro		
	380		385		390
Asn Tyr Pro Asp	Val Ile Tyr Glu Asp	Tyr Gly Thr Ala Ala	Asn		
	395		400		405
Asp Ile Gly Asp	Thr Thr Asn Arg Ser	Asn Glu Ile Pro Ser	Thr		
	410		415		420
Asp Val Thr Asp	Lys Thr Gly Arg Glu	His Leu Ser Val Tyr	Ala		
	425		430		435
Val Val Val Ile	Ala Ser Val Val Gly	Phe Cys Leu Leu Val	Met		
	440		445		450
Leu Phe Leu Leu	Lys Leu Ala Arg His	Ser Lys Phe Gly Met	Lys		
	455		460		465
Gly Pro Ala Ser	Val Ile Ser Asn Asp	Asp Asp Ser Ala Ser	Pro		
	470		475		480
Leu His His Ile	Ser Asn Gly Ser Asn	Thr Pro Ser Ser Ser	Glu		
	485		490		495
Gly Gly Pro Asp	Ala Val Ile Ile Gly	Met Thr Lys Ile Pro	Val		
	500		505		510
Ile Glu Asn Pro	Gln Tyr Phe Gly Ile	Thr Asn Ser Gln Leu	Lys		
	515		520		525
Pro Asp Thr Phe	Val Gln His Ile Lys	Arg His Asn Ile Val	Leu		
	530		535		540
Lys Arg Glu Leu	Gly Glu Gly Ala Phe	Gly Lys Val Phe Leu	Ala		
	545		550		555

Glu	Cys	Tyr	Asn	Leu	Cys	Pro	Glu	Gln	Asp	Lys	Ile	Leu	Val	Ala	560	565	570
Val	Lys	Thr	Leu	Lys	Asp	Ala	Ser	Asp	Asn	Ala	Arg	Lys	Asp	Phe	575	580	585
His	Arg	Glu	Ala	Glu	Leu	Leu	Thr	Asn	Leu	Gln	His	Glu	His	Ile	590	595	600
Val	Lys	Phe	Tyr	Gly	Val	Cys	Val	Glu	Gly	Asp	Pro	Leu	Ile	Met	605	610	615
Val	Phe	Glu	Tyr	Met	Lys	His	Gly	Asp	Leu	Asn	Lys	Phe	Leu	Arg	620	625	630
Ala	His	Gly	Pro	Asp	Ala	Val	Leu	Met	Ala	Glu	Gly	Asn	Pro	Pro	635	640	645
Thr	Glu	Leu	Thr	Gln	Ser	Gln	Met	Leu	His	Ile	Ala	Gln	Gln	Ile	650	655	660
Ala	Ala	Gly	Met	Val	Tyr	Leu	Ala	Ser	Gln	His	Phe	Val	His	Arg	665	670	675
Asp	Leu	Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Glu	Asn	Leu	Leu	Val	680	685	690
Lys	Ile	Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Val	Tyr	Ser	Thr	Asp	695	700	705
Tyr	Tyr	Arg	Val	Gly	Gly	His	Thr	Met	Leu	Pro	Ile	Arg	Trp	Met	710	715	720
Pro	Pro	Glu	Ser	Ile	Met	Tyr	Arg	Lys	Phe	Thr	Thr	Glu	Ser	Asp	725	730	735
Val	Trp	Ser	Leu	Gly	Val	Val	Leu	Trp	Glu	Ile	Phe	Thr	Tyr	Gly	740	745	750
Lys	Gln	Pro	Trp	Tyr	Gln	Leu	Ser	Asn	Asn	Glu	Val	Ile	Glu	Cys	755	760	765
Ile	Thr	Gln	Gly	Arg	Val	Leu	Gln	Arg	Pro	Arg	Thr	Cys	Pro	Gln	770	775	780
Glu	Val	Tyr	Glu	Leu	Met	Leu	Gly	Cys	Trp	Gln	Arg	Glu	Pro	His	785	790	795
Met	Arg	Lys	Asn	Ile	Lys	Gly	Ile	His	Thr	Leu	Leu	Gln	Asn	Leu	800	805	810

Ala Lys Ala Ser Pro Val Tyr Leu Asp Ile Leu Gly
815 820

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1870 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGAAGGTTTA AAGAAGAAGC CGCAAAGCGC AGGGAAGGCC TCCCGGCACG 50
GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100
CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150
CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200
TTCGCCTGTC CCACGTCCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250
CGACCCTTCT CCTGGCATCG TGGCATTTCC GAGATTGGAG CCTAACAGTG 300
TAGATCCTGA GAACATCACC GAAATTTTCA TCGCAAACCA GAAAAGGTTA 350
GAAATCATCA ACGAAGATGA TGTTGAAGCT TATGTGGGAC TGAGAAATCT 400
GACAATTGTG GATTCTGGAT TAAAATTTGT GGCTCATAAA GCATTTCTGA 450
AAAACAGCAA CCTGCAGCAC ATCAATTTTA CCCGAAACAA ACTGACGAGT 500
TTGTCTAGGA AACATTTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550
GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600
AAGAGGCTAA ATCCAGTCCA GAACTCAGG ATTTGTACTG CCTGAATGAA 650
AGCAGCAAGA ATATTCCCCT GGCAAACCTG CAGATACCCA ATTGTGGTTT 700
GCCATCTGCA AATCTGGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750
CTATCACATT ATCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800
TGGGATGTTG GTAACCTGGT TTCCAAACAT ATGAATGAAA CAAGCCACAC 850
ACAGGGCTCC TTAAGGATAA CTAACATTTT ATCCGATGAC AGTGGGAAGC 900
AGATCTCTTG TGTGGCGGAA AATCTTGTAG GAGAAGATCA AGATTCTGTC 950

AACCTCACTG TGCATTTTGC ACCAACTATC ACATTTCTCG AATCTCCAAC 1000
 CTCAGACCAC CACTGGTGCA TTCCATTAC TGTGAAAGGC AACCCAAAAC 1050
 CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAAATAC 1100
 ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150
 CCAGCTGGAT AATCCCACTC ACATGAACAA TGGGGACTAC ACTCTAATAG 1200
 CCAAGAATGA GTATGGGAAG GATGAGAAAC AGATTTCTGC TCACTTCATG 1250
 GGCTGGCCTG GAATTGACGA TGGTGCAAAC CCAAATTATC CTGATGTAAT 1300
 TTATGAAGAT TATGGAAGT CAGCGAATGA CATCGGGGAC ACCACGAACA 1350
 GAAGTAATGA AATCCCTTCC ACAGACGTCA CTGATAAAAC CGGTCGGGAA 1400
 CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTTG 1450
 CCTTTTGGTA ATGCTGTTTC TGCTTAAGTT GGCAAGACAC TCCAAGTTTG 1500
 GCATGAAAGG TTTTGTTTTG TTTCATAAGA TCCCACTGGA TGGGTAGCTG 1550
 AAATAAAGGA AAAGACAGAG AAAGGGGCTG TGGTGCTTGT TGGTTGATGC 1600
 TGCCATGTAA GCTGGACTCC TGGGACTGCT GTTGGCTTAT CCCGGGAAGT 1650
 GCTGCTTATC TGGGGTTTTT TGGTAGATGT GGGCGGTGTT TGGAGGCTGT 1700
 ACTATATGAA GCCTGCATAT ACTGTGAGCT GTGATTGGGG AACACCAATG 1750
 CAGAGGTAAC TCTCAGGCAG CTAAGCAGCA CCTCAAGAAA ACATGTTAAA 1800
 TTAATGCTTC TCTTCTTACA GTAGTTCAAA TACAAAACCTG AAATGAAATC 1850
 CCATTGGATT GTACTTCTCT 1870

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 477 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ser	Ser	Trp	Ile	Arg	Trp	His	Gly	Pro	Ala	Met	Ala	Arg	Leu
1				5					10					15
Trp	Gly	Phe	Cys	Trp	Leu	Val	Val	Gly	Phe	Trp	Arg	Ala	Ala	Phe
				20					25					30

Ala	Cys	Pro	Thr	Ser	Cys	Lys	Cys	Ser	Ala	Ser	Arg	Ile	Trp	Cys	
				35					40					45	
Ser	Asp	Pro	Ser	Pro	Gly	Ile	Val	Ala	Phe	Pro	Arg	Leu	Glu	Pro	
				50					55					60	
Asn	Ser	Val	Asp	Pro	Glu	Asn	Ile	Thr	Glu	Ile	Phe	Ile	Ala	Asn	
				65					70					75	
Gln	Lys	Arg	Leu	Glu	Ile	Ile	Asn	Glu	Asp	Asp	Val	Glu	Ala	Tyr	
				80					85					90	
Val	Gly	Leu	Arg	Asn	Leu	Thr	Ile	Val	Asp	Ser	Gly	Leu	Lys	Phe	
				95					100					105	
Val	Ala	His	Lys	Ala	Phe	Leu	Lys	Asn	Ser	Asn	Leu	Gln	His	Ile	
				110					115					120	
Asn	Phe	Thr	Arg	Asn	Lys	Leu	Thr	Ser	Leu	Ser	Arg	Lys	His	Phe	
				125					130					135	
Arg	His	Leu	Asp	Leu	Ser	Glu	Leu	Ile	Leu	Val	Gly	Asn	Pro	Phe	
				140					145					150	
Thr	Cys	Ser	Cys	Asp	Ile	Met	Trp	Ile	Lys	Thr	Leu	Gln	Glu	Ala	
				155					160					165	
Lys	Ser	Ser	Pro	Asp	Thr	Gln	Asp	Leu	Tyr	Cys	Leu	Asn	Glu	Ser	
				170					175					180	
Ser	Lys	Asn	Ile	Pro	Leu	Ala	Asn	Leu	Gln	Ile	Pro	Asn	Cys	Gly	
				185					190					195	
Leu	Pro	Ser	Ala	Asn	Leu	Ala	Ala	Pro	Asn	Leu	Thr	Val	Glu	Glu	
				200					205					210	
Gly	Lys	Ser	Ile	Thr	Leu	Ser	Cys	Ser	Val	Ala	Gly	Asp	Pro	Val	
				215					220					225	
Pro	Asn	Met	Tyr	Trp	Asp	Val	Gly	Asn	Leu	Val	Ser	Lys	His	Met	
				230					235					240	
Asn	Glu	Thr	Ser	His	Thr	Gln	Gly	Ser	Leu	Arg	Ile	Thr	Asn	Ile	
				245					250					255	
Ser	Ser	Asp	Asp	Ser	Gly	Lys	Gln	Ile	Ser	Cys	Val	Ala	Glu	Asn	
				260					265					270	
Leu	Val	Gly	Glu	Asp	Gln	Asp	Ser	Val	Asn	Leu	Thr	Val	His	Phe	
				275					280					285	

Ala	Pro	Thr	Ile	Thr	Phe	Leu	Glu	Ser	Pro	Thr	Ser	Asp	His	His	290	295	300
Trp	Cys	Ile	Pro	Phe	Thr	Val	Lys	Gly	Asn	Pro	Lys	Pro	Ala	Leu	305	310	315
Gln	Trp	Phe	Tyr	Asn	Gly	Ala	Ile	Leu	Asn	Glu	Ser	Lys	Tyr	Ile	320	325	330
Cys	Thr	Lys	Ile	His	Val	Thr	Asn	His	Thr	Glu	Tyr	His	Gly	Cys	335	340	345
Leu	Gln	Leu	Asp	Asn	Pro	Thr	His	Met	Asn	Asn	Gly	Asp	Tyr	Thr	350	355	360
Leu	Ile	Ala	Lys	Asn	Glu	Tyr	Gly	Lys	Asp	Glu	Lys	Gln	Ile	Ser	365	370	375
Ala	His	Phe	Met	Gly	Trp	Pro	Gly	Ile	Asp	Asp	Gly	Ala	Asn	Pro	380	385	390
Asn	Tyr	Pro	Asp	Val	Ile	Tyr	Glu	Asp	Tyr	Gly	Thr	Ala	Ala	Asn	395	400	405
Asp	Ile	Gly	Asp	Thr	Thr	Asn	Arg	Ser	Asn	Glu	Ile	Pro	Ser	Thr	410	415	420
Asp	Val	Thr	Asp	Lys	Thr	Gly	Arg	Glu	His	Leu	Ser	Val	Tyr	Ala	425	430	435
Val	Val	Val	Ile	Ala	Ser	Val	Val	Gly	Phe	Cys	Leu	Leu	Val	Met	440	445	450
Leu	Phe	Leu	Leu	Lys	Leu	Ala	Arg	His	Ser	Lys	Phe	Gly	Met	Lys	455	460	465
Gly	Phe	Val	Leu	Phe	His	Lys	Ile	Pro	Leu	Asp	Gly				470	475	

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2715 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGATCCGCGT CGGAGATGGA TGTCTCTCTT TGCCCAGCCA AGTGTAGTTT 50

CTGGCGGATT TTCTTGCTGG GAAGCGTCTG GCTGGACTAT GTGGGCTCCG 100
 TGCTGGCTTG CCCTGCAAAT TGTGTCTGCA GCAAGACTGA GATCAATTGC 150
 CGGCGGCCGG ACGATGGGAA CCTCTTCCCC CTCCTGGAAG GGCAGGATTC 200
 AGGGAACAGC AATGGGAACG CCAATATCAA CATCACGGAC ATCTCAAGGA 250
 ATATCACTTC CATAACATA GAGAACTGGC GCAGTCTTCA CACGCTCAAC 300
 GCCGTGGACA TGGAGCTCTA CACCGGACTT CAAAAGCTGA CCATCAAGAA 350
 CTCAGGACTT CGGAGCATTC AGCCCAGAGC CTTTGCCAAG AACCCCCATT 400
 TGC GTTATAT AAACCTGTCA AGTAACCGGC TCACCACACT CTCGTGGCAG 450
 CTCTTCCAGA CGCTGAGTCT TCGGGAATTG CAGTTGGAGC AGAACTTTTT 500
 CAACTGCAGC TGTGACATCC GCTGGATGCA GCTCTGGCAG GAGCAGGGGG 550
 AGGCCAAGCT CAACAGCCAG AACCTCTACT GCATCAATGC TGATGGCTCC 600
 CAGCTTCCTC TCTTCCGCAT GAACATCAGT CAGTGTGACC TTCCTGAGAT 650
 CAGCGTGAGC CACGTCAACC TGACCGTACG AGAGGGTGAC AATGCTGTTA 700
 TCACTTGCAA TGGCTCTGGA TCACCCCTTC CTGATGTGGA CTGGATAGTC 750
 ACTGGGCTGC AGTCCATCAA CACTCACCAG ACCAATCTGA ACTGGACCAA 800
 TGTTTCATGCC ATCAACTTGA CGCTGGTGAA TGTGACGAGT GAGGACAATG 850
 GCTTCACCTT GACGTGCATT GCAGAGAACG TGGTGGGCAT GAGCAATGCC 900
 AGTGTGCCC TCACTGTCTA CTATCCCCCA CGTGTGGTGA GCCTGGAGGA 950
 GCCTGAGCTG CGCCTGGAGC ACTGCATCGA GTTTGTGGTG CGTGGCAACC 1000
 CCCACCAAC GCTGCACTGG CTGCACAATG GGCAGCCTCT GCGGGAGTCC 1050
 AAGATCATCC ATGTGGAATA CTACCAAGAG GGAGAGATTT CCGAGGGCTG 1100
 CCTGCTCTTC AACAAAGCCCA CCCACTACAA CAATGGCAAC TATACCCTCA 1150
 TTGCCAAAAA CCCACTGGGC ACAGCCAACC AGACCATCAA TGGCCACTTC 1200
 CTCAAGGAGC CCTTTCCAGA GAGCACGGAT AACTTTATCT TGTTTGACGA 1250
 AGTGAGTCCC ACACCTCCTA TCACTGTGAC CCACAAACCA GAAGAAGACA 1300
 CTTTTGGGGT ATCCATAGCA GTTGGACTTG CTGCTTTTGC CTGTGTCCTG 1350

TTGGTGGTTC TCTTCGTCAT GATCAACAAA TATGGTCGAC GGTCCAAATT 1400
 TGGAATGAAG GGTCCCGTGG CTGTCATCAG TGGTGAGGAG GACTCAGCCA 1450
 GCCCACTGCA CCACATCAAC CACGGCATCA CCACGCCCTC GTCACTGGAT 1500
 GCCGGGCCCCG AACTGTGGT CATTGGCATG ACTCGCATCC CTGTCATTGA 1550
 GAACCCCCAG TACTTCCGTC AGGGACACAA CTGCCACAAG CCGGACACGT 1600
 ATGTGCAGCA CATTAAGAGG AGAGACATCG TGCTGAAGCG AGAACTGGGT 1650
 GAGGGAGCCT TTGGAAAGGT CTCCTGGCC GAGTGCTACA ACCTCAGCCC 1700
 GACCAAGGAC AAGATGCTTG TGGCTGTGAA GGCCCTGAAG GATCCCACCC 1750
 TGGCTGCCCCG GAAGGATTTT CAGAGGGAGG CCGAGCTGCT CACCAACCTG 1800
 CAGCATGAGC ACATTGTCAA GTTCTATGGA GTGTGCGGCG ATGGGGACCC 1850
 CCTCATCATG GTCTTTGAAT ACATGAAGCA TGGAGACCTG AATAAGTTCC 1900
 TCAGGGCCCA TGGGCCAGAT GCAATGATCC TTGTGGATGG ACAGCCACGC 1950
 CAGGCCAAGG GTGAGCTGGG GCTCTCCCAA ATGCTCCACA TTGCCAGTCA 2000
 GATCGCCTCG GGTATGGTGT ACCTGGCCTC CCAGCACTTT GTGCACCGAG 2050
 ACCTGGCCAC CAGGAACTGC CTGGTTGGAG CGAATCTGCT AGTGAAGATT 2100
 GGGGACTTCG GCATGTCCAG AGATGTCTAC AGCACGGATT ATTACAGGCT 2150
 CTTTAATCCA TCTGGAAATG ATTTTGTAT ATGGTGTGAG GTGGGAGGAC 2200
 ACACCATGCT CCCCATTCGC TGGATGCCTC CTGAAAGCAT CATGTACCGG 2250
 AAGTTCACTA CAGAGAGTGA TGTATGGAGC TTCGGGGTGA TCCTCTGGGA 2300
 GATCTTCACC TATGGAAAGC AGCCATGGTT CCAACTCTCA AACACGGAGG 2350
 TCATTGAGTG CATTACCCAA GGTCGTGTTT TGGAGCGGCC CCGAGTCTGC 2400
 CCCAAAGAGG TGTACGATGT CATGCTGGGG TGCTGGCAGA GGGAACCACA 2450
 GCAGCGGTTG AACATCAAGG AGATCTACAA AATCCTCCAT GCTTTGGGGA 2500
 AGGCCACCCC AATCTACCTG GACATTCTTG GCTAGTGGTG GCTGGTGGTC 2550
 ATGAATTCAT ACTCTGTTGC CTCCTCTCTC CCTGCCTCAC ATCTCCCTTC 2600
 CACCTCACAA CTCCTTCCAT CCTTGACTGA AGCGAACATC TTCATATAAA 2650

CTCAAGTGCC TGCTACACAT ACAACACTGA AAAAAGGAAA AAAAAAGAAA 2700
 AAAAAAAAAA ACCGC 2715

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 839 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Val	Ser	Leu	Cys	Pro	Ala	Lys	Cys	Ser	Phe	Trp	Arg	Ile	1	5	10	15
Phe	Leu	Leu	Gly	Ser	Val	Trp	Leu	Asp	Tyr	Val	Gly	Ser	Val	Leu	20	25	30	
Ala	Cys	Pro	Ala	Asn	Cys	Val	Cys	Ser	Lys	Thr	Glu	Ile	Asn	Cys	35	40	45	
Arg	Arg	Pro	Asp	Asp	Gly	Asn	Leu	Phe	Pro	Leu	Leu	Glu	Gly	Gln	50	55	60	
Asp	Ser	Gly	Asn	Ser	Asn	Gly	Asn	Ala	Asn	Ile	Asn	Ile	Thr	Asp	65	70	75	
Ile	Ser	Arg	Asn	Ile	Thr	Ser	Ile	His	Ile	Glu	Asn	Trp	Arg	Ser	80	85	90	
Leu	His	Thr	Leu	Asn	Ala	Val	Asp	Met	Glu	Leu	Tyr	Thr	Gly	Leu	95	100	105	
Gln	Lys	Leu	Thr	Ile	Lys	Asn	Ser	Gly	Leu	Arg	Ser	Ile	Gln	Pro	110	115	120	
Arg	Ala	Phe	Ala	Lys	Asn	Pro	His	Leu	Arg	Tyr	Ile	Asn	Leu	Ser	125	130	135	
Ser	Asn	Arg	Leu	Thr	Thr	Leu	Ser	Trp	Gln	Leu	Phe	Gln	Thr	Leu	140	145	150	
Ser	Leu	Arg	Glu	Leu	Gln	Leu	Glu	Gln	Asn	Phe	Phe	Asn	Cys	Ser	155	160	165	
Cys	Asp	Ile	Arg	Trp	Met	Gln	Leu	Trp	Gln	Glu	Gln	Gly	Glu	Ala	170	175	180	
Lys	Leu	Asn	Ser	Gln	Asn	Leu	Tyr	Cys	Ile	Asn	Ala	Asp	Gly	Ser	185	190	195	

Gln	Leu	Pro	Leu	Phe	Arg	Met	Asn	Ile	Ser	Gln	Cys	Asp	Leu	Pro
				200					205					210
Glu	Ile	Ser	Val	Ser	His	Val	Asn	Leu	Thr	Val	Arg	Glu	Gly	Asp
				215					220					225
Asn	Ala	Val	Ile	Thr	Cys	Asn	Gly	Ser	Gly	Ser	Pro	Leu	Pro	Asp
				230					235					240
Val	Asp	Trp	Ile	Val	Thr	Gly	Leu	Gln	Ser	Ile	Asn	Thr	His	Gln
				245					250					255
Thr	Asn	Leu	Asn	Trp	Thr	Asn	Val	His	Ala	Ile	Asn	Leu	Thr	Leu
				260					265					270
Val	Asn	Val	Thr	Ser	Glu	Asp	Asn	Gly	Phe	Thr	Leu	Thr	Cys	Ile
				275					280					285
Ala	Glu	Asn	Val	Val	Gly	Met	Ser	Asn	Ala	Ser	Val	Ala	Leu	Thr
				290					295					300
Val	Tyr	Tyr	Pro	Pro	Arg	Val	Val	Ser	Leu	Glu	Glu	Pro	Glu	Leu
				305					310					315
Arg	Leu	Glu	His	Cys	Ile	Glu	Phe	Val	Val	Arg	Gly	Asn	Pro	Pro
				320					325					330
Pro	Thr	Leu	His	Trp	Leu	His	Asn	Gly	Gln	Pro	Leu	Arg	Glu	Ser
				335					340					345
Lys	Ile	Ile	His	Val	Glu	Tyr	Tyr	Gln	Glu	Gly	Glu	Ile	Ser	Glu
				350					355					360
Gly	Cys	Leu	Leu	Phe	Asn	Lys	Pro	Thr	His	Tyr	Asn	Asn	Gly	Asn
				365					370					375
Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Pro	Leu	Gly	Thr	Ala	Asn	Gln	Thr
				380					385					390
Ile	Asn	Gly	His	Phe	Leu	Lys	Glu	Pro	Phe	Pro	Glu	Ser	Thr	Asp
				395					400					405
Asn	Phe	Ile	Leu	Phe	Asp	Glu	Val	Ser	Pro	Thr	Pro	Pro	Ile	Thr
				410					415					420
Val	Thr	His	Lys	Pro	Glu	Glu	Asp	Thr	Phe	Gly	Val	Ser	Ile	Ala
				425					430					435
Val	Gly	Leu	Ala	Ala	Phe	Ala	Cys	Val	Leu	Leu	Val	Val	Leu	Phe
				440					445					450
Val	Met	Ile	Asn	Lys	Tyr	Gly	Arg	Arg	Ser	Lys	Phe	Gly	Met	Lys

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	455		460		465
Gly Pro Val Ala	Val Ile Ser Gly Glu	Glu Asp Ser Ala Ser	Pro		
	470		475		480
Leu His His Ile	Asn His Gly Ile Thr	Thr Pro Ser Ser Leu	Asp		
	485		490		495
Ala Gly Pro Asp	Thr Val Val Ile Gly	Met Thr Arg Ile Pro	Val		
	500		505		510
Ile Glu Asn Pro	Gln Tyr Phe Arg Gln	Gly His Asn Cys His	Lys		
	515		520		525
Pro Asp Thr Tyr	Val Gln His Ile Lys	Arg Arg Asp Ile Val	Leu		
	530		535		540
Lys Arg Glu Leu	Gly Glu Gly Ala Phe	Gly Lys Val Phe Leu	Ala		
	545		550		555
Glu Cys Tyr Asn	Leu Ser Pro Thr Lys	Asp Lys Met Leu Val	Ala		
	560		565		570
Val Lys Ala Leu	Lys Asp Pro Thr Leu	Ala Ala Arg Lys Asp	Phe		
	575		580		585
Gln Arg Glu Ala	Glu Leu Leu Thr Asn	Leu Gln His Glu His	Ile		
	590		595		600
Val Lys Phe Tyr	Gly Val Cys Gly Asp	Gly Asp Pro Leu Ile	Met		
	605		610		615
Val Phe Glu Tyr	Met Lys His Gly Asp	Leu Asn Lys Phe Leu	Arg		
	620		625		630
Ala His Gly Pro	Asp Ala Met Ile Leu	Val Asp Gly Gln Pro	Arg		
	635		640		645
Gln Ala Lys Gly	Glu Leu Gly Leu Ser	Gln Met Leu His Ile	Ala		
	650		655		660
Ser Gln Ile Ala	Ser Gly Met Val Tyr	Leu Ala Ser Gln His	Phe		
	665		670		675
Val His Arg Asp	Leu Ala Thr Arg Asn	Cys Leu Val Gly Ala	Asn		
	680		685		690
Leu Leu Val Lys	Ile Gly Asp Phe Gly	Met Ser Arg Asp Val	Tyr		
	695		700		705
Ser Thr Asp Tyr	Tyr Arg Leu Phe Asn	Pro Ser Gly Asn Asp	Phe		
	710		715		720

Cys	Ile	Trp	Cys	Glu	Val	Gly	Gly	His	Thr	Met	Leu	Pro	Ile	Arg
				725					730					735
Trp	Met	Pro	Pro	Glu	Ser	Ile	Met	Tyr	Arg	Lys	Phe	Thr	Thr	Glu
				740					745					750
Ser	Asp	Val	Trp	Ser	Phe	Gly	Val	Ile	Leu	Trp	Glu	Ile	Phe	Thr
				755					760					765
Tyr	Gly	Lys	Gln	Pro	Trp	Phe	Gln	Leu	Ser	Asn	Thr	Glu	Val	Ile
				770					775					780
Glu	Cys	Ile	Thr	Gln	Gly	Arg	Val	Leu	Glu	Arg	Pro	Arg	Val	Cys
				785					790					795
Pro	Lys	Glu	Val	Tyr	Asp	Val	Met	Leu	Gly	Cys	Trp	Gln	Arg	Glu
				800					805					810
Pro	Gln	Gln	Arg	Leu	Asn	Ile	Lys	Glu	Ile	Tyr	Lys	Ile	Leu	His
				815					820					825
Ala	Leu	Gly	Lys	Ala	Thr	Pro	Ile	Tyr	Leu	Asp	Ile	Leu	Gly	
				830					835					

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1858 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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GGATCCGCGT CGGAGATGGA TGTCTCTCTT TGCCCAGCCA AGTGTAGTTT 50
CTGGCGGATT TTCTTGCTGG GAAGCGTCTG GCTGGACTAT GTGGGCTCCG 100
TGCTGGCTTG CCCTGCAAAT TGTGTCTGCA GCAAGACTGA GATCAATTGC 150
CGGCGGCCCG ACGATGGGAA CCTCTTCCCC CTCCTGGAAG GGCAGGATTC 200
AGGGAACAGC AATGGGAACG CCAATATCAA CATCACGGAC ATCTCAAGGA 250
ATATCACTTC CATAACATA GAGAACTGGC GCAGTCTTCA CACGCTCAAC 300
GCCGTGGACA TGGAGCTCTA CACCGGACTT CAAAAGCTGA CCATCAAGAA 350
CTCAGGACTT CGGAGCATTC AGCCCAGAGC CTTTGCCAAG AACCCCCATT 400

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TCGGTTATAT AAACCTGTCA AGTAACCGGC TCACCACACT CTCGTGGCAG 450
 CTCTTCCAGA CGCTGAGTCT TCGGGAATTG CAGTTGGAGC AGAACTTTTT 500
 CAACTGCAGC TGTGACATCC GCTGGATGCA GCTCTGGCAG GAGCAGGGGG 550
 AGGCCAAGCT CAACAGCCAG AACCTCTACT GCATCAATGC TGATGGCTCC 600
 CAGCTTCCTC TCTTCCGCAT GAACATCAGT CAGTGTGACC TTCCTGAGAT 650
 CAGCGTGAGC CACGTCAACC TGACCGTACG AGAGGGTGAC AATGCTGTTA 700
 TCACTTGCAA TGGCTCTGGA TCACCCCTTC CTGATGTGGA CTGGATAGTC 750
 ACTGGGCTGC AGTCCATCAA CACTCACCAG ACCAATCTGA ACTGGACCAA 800
 TGTTTCATGCC ATCAACTTGA CGCTGGTGAA TGTGACGAGT GAGGACAATG 850
 GCTTCACCTT GACGTGCATT GCAGAGAACG TGGTGGGCAT GAGCAATGCC 900
 AGTGTTGCCC TCACTGTCTA CTATCCCCCA CGTGTGGTGA GCCTGGAGGA 950
 GCCTGAGCTG CGCCTGGAGC ACTGCATCGA GTTTGTGGTG CGTGGCAACC 1000
 CCCCACCAAC GCTGCACTGG CTGCACAATG GGCAGCCTCT GCGGGAGTCC 1050
 AAGATCATCC ATGTGGAATA CTACCAAGAG GGAGAGATTT CCGAGGGCTG 1100
 CCTGCTCTTC AACAAGCCCA CCCACTACAA CAATGGCAAC TATACCCTCA 1150
 TTGCCAAAAA CCCACTGGGC ACAGCCAACC AGACCATCAA TGGCCACTTC 1200
 CTCAAGGAGC CCTTTCCAGA GAGCACGGAT AACTTTATCT TGTTTGACGA 1250
 AGTGAGTCCC ACACCTCCTA TCACTGTGAC CCACAAACCA GAAGAAGACA 1300
 CTTTTGGGGT ATCCATAGCA GTTGGACTTG CTGCTTTTGC CTGTGTCCTG 1350
 TTGGTGGTTC TCTTCGTCAT GATCAACAAA TATGGTCGAC GGTCCAAATT 1400
 TGGAATGAAG GGTCCCGTGG CTGTCATCAG TGGTGAGGAG GACTCAGCCA 1450
 GCCCACTGCA CCACATCAAC CACGGCATCA CCACGCCCTC GTCACTGGAT 1500
 GCCGGGCCCCG ACACTGTGGT CATTGGCATG ACTCGCATCC CTGTCATTGA 1550
 GAACCCCCAG TACTTCCGTC AGGGACACAA CTGCCACAAG CCGGACACGT 1600
 GGGTCTTTTC AAACATAGAC AATCATGGGA TATTAACTT GAAGGACAAT 1650
 AGAGATCATC TAGTCCCATC AACTCACTAT ATATATGAGG AACCTGAGGT 1700

CCAGAGTGGG GAAGTGTCTT ACCCAAGGTC ACATGGTTTC AGAGAAATTA 1750
 TGTGAATCC AATAAGCCTT CCCGGACATT CCAAGCCTCT TAACCATGGC 1800
 ATCTATGTTG AGGATGTCAA TGTTTATTTT AGCAAAGGAC GTCATGGCCT 1850
 TTAAAAAC 1858

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 612 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Asp	Val	Ser	Leu	Cys	Pro	Ala	Lys	Cys	Ser	Phe	Trp	Arg	Ile	1	5	10	15
Phe	Leu	Leu	Gly	Ser	Val	Trp	Leu	Asp	Tyr	Val	Gly	Ser	Val	Leu	20	25	30	
Ala	Cys	Pro	Ala	Asn	Cys	Val	Cys	Ser	Lys	Thr	Glu	Ile	Asn	Cys	35	40	45	
Arg	Arg	Pro	Asp	Asp	Gly	Asn	Leu	Phe	Pro	Leu	Leu	Glu	Gly	Gln	50	55	60	
Asp	Ser	Gly	Asn	Ser	Asn	Gly	Asn	Ala	Asn	Ile	Asn	Ile	Thr	Asp	65	70	75	
Ile	Ser	Arg	Asn	Ile	Thr	Ser	Ile	His	Ile	Glu	Asn	Trp	Arg	Ser	80	85	90	
Leu	His	Thr	Leu	Asn	Ala	Val	Asp	Met	Glu	Leu	Tyr	Thr	Gly	Leu	95	100	105	
Gln	Lys	Leu	Thr	Ile	Lys	Asn	Ser	Gly	Leu	Arg	Ser	Ile	Gln	Pro	110	115	120	
Arg	Ala	Phe	Ala	Lys	Asn	Pro	His	Leu	Arg	Tyr	Ile	Asn	Leu	Ser	125	130	135	
Ser	Asn	Arg	Leu	Thr	Thr	Leu	Ser	Trp	Gln	Leu	Phe	Gln	Thr	Leu	140	145	150	
Ser	Leu	Arg	Glu	Leu	Gln	Leu	Glu	Gln	Asn	Phe	Phe	Asn	Cys	Ser	155	160	165	
Cys	Asp	Ile	Arg	Trp	Met	Gln	Leu	Trp	Gln	Glu	Gln	Gly	Glu	Ala	170	175	180	

Lys	Leu	Asn	Ser	Gln	Asn	Leu	Tyr	Cys	Ile	Asn	Ala	Asp	Gly	Ser	185	190	195
Gln	Leu	Pro	Leu	Phe	Arg	Met	Asn	Ile	Ser	Gln	Cys	Asp	Leu	Pro	200	205	210
Glu	Ile	Ser	Val	Ser	His	Val	Asn	Leu	Thr	Val	Arg	Glu	Gly	Asp	215	220	225
Asn	Ala	Val	Ile	Thr	Cys	Asn	Gly	Ser	Gly	Ser	Pro	Leu	Pro	Asp	230	235	240
Val	Asp	Trp	Ile	Val	Thr	Gly	Leu	Gln	Ser	Ile	Asn	Thr	His	Gln	245	250	255
Thr	Asn	Leu	Asn	Trp	Thr	Asn	Val	His	Ala	Ile	Asn	Leu	Thr	Leu	260	265	270
Val	Asn	Val	Thr	Ser	Glu	Asp	Asn	Gly	Phe	Thr	Leu	Thr	Cys	Ile	275	280	285
Ala	Glu	Asn	Val	Val	Gly	Met	Ser	Asn	Ala	Ser	Val	Ala	Leu	Thr	290	295	300
Val	Tyr	Tyr	Pro	Pro	Arg	Val	Val	Ser	Leu	Glu	Glu	Pro	Glu	Leu	305	310	315
Arg	Leu	Glu	His	Cys	Ile	Glu	Phe	Val	Val	Arg	Gly	Asn	Pro	Pro	320	325	330
Pro	Thr	Leu	His	Trp	Leu	His	Asn	Gly	Gln	Pro	Leu	Arg	Glu	Ser	335	340	345
Lys	Ile	Ile	His	Val	Glu	Tyr	Tyr	Gln	Glu	Gly	Glu	Ile	Ser	Glu	350	355	360
Gly	Cys	Leu	Leu	Phe	Asn	Lys	Pro	Thr	His	Tyr	Asn	Asn	Gly	Asn	365	370	375
Tyr	Thr	Leu	Ile	Ala	Lys	Asn	Pro	Leu	Gly	Thr	Ala	Asn	Gln	Thr	380	385	390
Ile	Asn	Gly	His	Phe	Leu	Lys	Glu	Pro	Phe	Pro	Glu	Ser	Thr	Asp	395	400	405
Asn	Phe	Ile	Leu	Phe	Asp	Glu	Val	Ser	Pro	Thr	Pro	Pro	Ile	Thr	410	415	420
Val	Thr	His	Lys	Pro	Glu	Glu	Asp	Thr	Phe	Gly	Val	Ser	Ile	Ala	425	430	435

Val	Gly	Leu	Ala	Ala	Phe	Ala	Cys	Val	Leu	Leu	Val	Val	Leu	Phe	440	445	450
Val	Met	Ile	Asn	Lys	Tyr	Gly	Arg	Arg	Ser	Lys	Phe	Gly	Met	Lys	455	460	465
Gly	Pro	Val	Ala	Val	Ile	Ser	Gly	Glu	Glu	Asp	Ser	Ala	Ser	Pro	470	475	480
Leu	His	His	Ile	Asn	His	Gly	Ile	Thr	Thr	Pro	Ser	Ser	Leu	Asp	485	490	495
Ala	Gly	Pro	Asp	Thr	Val	Val	Ile	Gly	Met	Thr	Arg	Ile	Pro	Val	500	505	510
Ile	Glu	Asn	Pro	Gln	Tyr	Phe	Arg	Gln	Gly	His	Asn	Cys	His	Lys	515	520	525
Pro	Asp	Thr	Trp	Val	Phe	Ser	Asn	Ile	Asp	Asn	His	Gly	Ile	Leu	530	535	540
Asn	Leu	Lys	Asp	Asn	Arg	Asp	His	Leu	Val	Pro	Ser	Thr	His	Tyr	545	550	555
Ile	Tyr	Glu	Glu	Pro	Glu	Val	Gln	Ser	Gly	Glu	Val	Ser	Tyr	Pro	560	565	570
Arg	Ser	His	Gly	Phe	Arg	Glu	Ile	Met	Leu	Asn	Pro	Ile	Ser	Leu	575	580	585
Pro	Gly	His	Ser	Lys	Pro	Leu	Asn	His	Gly	Ile	Tyr	Val	Glu	Asp	590	595	600
Val	Asn	Val	Tyr	Phe	Ser	Lys	Gly	Arg	His	Gly	Phe				605	610	

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 790 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Leu	Arg	Gly	Gly	Arg	Arg	Gly	Gln	Leu	Gly	Trp	His	Ser	Trp	1	5	10	15
Ala	Ala	Gly	Pro	Gly	Ser	Leu	Leu	Ala	Trp	Leu	Ile	Leu	Ala	Ser	20	25	30	
Ala	Gly	Ala	Ala	Pro	Cys	Pro	Asp	Ala	Cys	Cys	Pro	His	Gly	Ser				

35					40					45				
Ser	Gly	Leu	Arg	Cys	Thr	Arg	Asp	Gly	Ala	Leu	Asp	Ser	Leu	His
				50					55					60
His	Leu	Pro	Gly	Ala	Glu	Asn	Leu	Thr	Glu	Leu	Tyr	Ile	Glu	Asn
				65					70					75
Gln	Gln	His	Leu	Gln	His	Leu	Glu	Leu	Arg	Asp	Leu	Arg	Gly	Leu
				80					85					90
Gly	Glu	Leu	Arg	Asn	Leu	Thr	Ile	Val	Lys	Ser	Gly	Leu	Arg	Phe
				95					100					105
Val	Ala	Pro	Asp	Ala	Phe	His	Phe	Thr	Pro	Arg	Leu	Ser	Arg	Leu
				110					115					120
Asn	Leu	Ser	Phe	Asn	Ala	Leu	Glu	Ser	Leu	Ser	Trp	Lys	Thr	Val
				125					130					135
Gln	Gly	Leu	Ser	Leu	Gln	Glu	Leu	Val	Leu	Ser	Gly	Asn	Pro	Leu
				140					145					150
His	Cys	Ser	Cys	Ala	Leu	Arg	Trp	Leu	Gln	Arg	Trp	Glu	Glu	Glu
				155					160					165
Gly	Leu	Gly	Gly	Val	Pro	Glu	Gln	Lys	Leu	Gln	Cys	His	Gly	Gln
				170					175					180
Gly	Pro	Leu	Ala	His	Met	Pro	Asn	Ala	Ser	Cys	Gly	Val	Pro	Thr
				185					190					195
Leu	Lys	Val	Gln	Val	Pro	Asn	Ala	Ser	Val	Asp	Val	Gly	Asp	Asp
				200					205					210
Val	Leu	Leu	Arg	Cys	Gln	Val	Glu	Gly	Arg	Gly	Leu	Glu	Gln	Ala
				215					220					225
Gly	Trp	Ile	Leu	Thr	Glu	Leu	Glu	Gln	Ser	Ala	Thr	Val	Met	Lys
				230					235					240
Ser	Gly	Gly	Leu	Pro	Ser	Leu	Gly	Leu	Thr	Leu	Ala	Asn	Val	Thr
				245					250					255
Ser	Asp	Leu	Asn	Arg	Lys	Asn	Leu	Thr	Cys	Trp	Ala	Glu	Asn	Asp
				260					265					270
Val	Gly	Arg	Ala	Glu	Val	Ser	Val	Gln	Val	Asn	Val	Ser	Phe	Pro
				275					280					285
Ala	Ser	Val	Gln	Leu	His	Thr	Ala	Val	Glu	Met	His	His	Trp	Cys
				290					295					300

Ile	Pro	Phe	Ser	Val	Asp	Gly	Gln	Pro	Ala	Pro	Ser	Leu	Arg	Trp	305	310	315
Leu	Phe	Asn	Gly	Ser	Val	Leu	Asn	Glu	Thr	Ser	Phe	Ile	Phe	Thr	320	325	330
Glu	Phe	Leu	Glu	Pro	Ala	Ala	Asn	Glu	Thr	Val	Arg	His	Gly	Cys	335	340	345
Leu	Arg	Leu	Asn	Gln	Pro	Thr	His	Val	Asn	Asn	Gly	Asn	Tyr	Thr	350	355	360
Leu	Leu	Ala	Ala	Asn	Pro	Phe	Gly	Gln	Ala	Ser	Ala	Ser	Ile	Met	365	370	375
Ala	Ala	Phe	Met	Asp	Asn	Pro	Phe	Glu	Phe	Asn	Pro	Glu	Asp	Pro	380	385	390
Ile	Pro	Asp	Thr	Asn	Ser	Thr	Ser	Gly	Asp	Pro	Val	Glu	Lys	Lys	395	400	405
Asp	Glu	Thr	Pro	Phe	Gly	Val	Ser	Val	Ala	Val	Gly	Leu	Ala	Val	410	415	420
Phe	Ala	Cys	Leu	Phe	Leu	Ser	Thr	Leu	Leu	Leu	Val	Leu	Asn	Lys	425	430	435
Cys	Gly	Arg	Arg	Asn	Lys	Phe	Gly	Ile	Asn	Arg	Pro	Ala	Val	Leu	440	445	450
Ala	Pro	Glu	Asp	Gly	Leu	Ala	Met	Ser	Leu	His	Phe	Met	Thr	Leu	455	460	465
Gly	Gly	Ser	Ser	Leu	Ser	Pro	Thr	Glu	Gly	Lys	Gly	Ser	Gly	Leu	470	475	480
Gln	Gly	His	Ile	Ile	Glu	Asn	Pro	Gln	Tyr	Phe	Ser	Asp	Ala	Cys	485	490	495
Val	His	His	Ile	Lys	Arg	Arg	Asp	Ile	Val	Leu	Lys	Trp	Glu	Leu	500	505	510
Gly	Glu	Gly	Ala	Phe	Gly	Lys	Val	Phe	Leu	Ala	Glu	Cys	His	Asn	515	520	525
Leu	Leu	Pro	Glu	Gln	Asp	Lys	Met	Leu	Val	Ala	Val	Lys	Ala	Leu	530	535	540
Lys	Glu	Ala	Ser	Glu	Ser	Ala	Arg	Gln	Asp	Phe	Gln	Arg	Glu	Ala	545	550	555

Glu	Leu	Leu	Thr	Met	Leu	Gln	His	Gln	His	Ile	Val	Arg	Phe	Phe
				560					565					570
Gly	Val	Cys	Thr	Glu	Gly	Arg	Pro	Leu	Leu	Met	Val	Phe	Glu	Tyr
				575					580					585
Met	Arg	His	Gly	Asp	Leu	Asn	Arg	Phe	Leu	Arg	Ser	His	Gly	Pro
				590					595					600
Asp	Ala	Lys	Leu	Leu	Ala	Gly	Gly	Glu	Asp	Val	Ala	Pro	Gly	Pro
				605					610					615
Leu	Gly	Leu	Gly	Gln	Leu	Leu	Ala	Val	Ala	Ser	Gln	Val	Ala	Ala
				620					625					630
Gly	Met	Val	Tyr	Leu	Ala	Gly	Leu	His	Phe	Val	His	Arg	Asp	Leu
				635					640					645
Ala	Thr	Arg	Asn	Cys	Leu	Val	Gly	Gln	Gly	Leu	Val	Val	Lys	Ile
				650					655					660
Gly	Asp	Phe	Gly	Met	Ser	Arg	Asp	Ile	Tyr	Ser	Thr	Asp	Tyr	Tyr
				665					670					675
Arg	Val	Gly	Gly	Arg	Thr	Met	Leu	Pro	Ile	Arg	Trp	Met	Pro	Pro
				680					685					690
Glu	Ser	Ile	Leu	Tyr	Arg	Lys	Phe	Thr	Thr	Glu	Ser	Asp	Val	Trp
				695					700					705
Ser	Phe	Gly	Val	Val	Leu	Trp	Glu	Ile	Phe	Thr	Tyr	Gly	Lys	Gln
				710					715					720
Pro	Trp	Tyr	Gln	Leu	Ser	Asn	Thr	Glu	Ala	Ile	Asp	Cys	Ile	Thr
				725					730					735
Gln	Gly	Arg	Glu	Leu	Glu	Arg	Pro	Arg	Ala	Cys	Pro	Pro	Glu	Val
				740					745					750
Tyr	Ala	Ile	Met	Arg	Gly	Cys	Trp	Gln	Arg	Glu	Pro	Gln	Gln	Arg
				755					760					765
His	Ser	Ile	Lys	Asp	Val	His	Ala	Arg	Leu	Gln	Ala	Leu	Ala	Gln
				770					775					780
Ala	Pro	Pro	Val	Tyr	Leu	Asp	Val	Leu	Gly					
				785					790					

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGYGAYATHA TGTGGYTNAAC RAC 23

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGATGCARY TNTGGCARCA RCA 23

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

YTCRTCYTTN CCRTAYTCRT T 21

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCYTCYTGRT ARTAYTCNAC GTG 23

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CACGTCAACA ACGGCAACTA CA 22

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAAGGATGA GAAACAGATT TCTGC 25

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CATCAATGGC CACTTCTCTCA AGG 23

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGGTGTTTCG TCCTTCTTCT CC 22

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAGATGTGCC CGACCGGTTG TATC 24

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CACAGTGATA GGAGGTGTGG GA 22

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATGTGGCT CCAGGCCCC 19

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGGCAACCCG CCCACGGAA 19

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACGCCAGGCC AAGGGTGAG 19

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAACCACTCC CAGCCCCTGG 20

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTGGTGGCCT CCAGCGGCAG 20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AATTCATGAC CACCAGCCAC CA 22

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCTCCTCGGG ACTGCGATGC 20

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATGTCGCCCT GGCCGAGGTG GCAT 24

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AAGCTCAACA GCCAGAACCT C 21

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAGCTCTGTG AGGATCCAGC C 21

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCGACCGGTT TTATCAGTGA C 21

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGATCTTGG ACTCCCGCAG AGG 23

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTTGGCCAAG GCATCTCCGG T 21

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGTGCAGCA CATTAAGAGG A 21

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs

- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTATACACAG GCTTAAGCCA TCCA 24

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGGAGGCATC CAGCGAATG 19

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Glu Ser Thr Asp Asn Phe Ile Leu Phe
1 5

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Leu Phe Asn Pro Ser Gly Asn Asp Phe Cys Ile Trp Cys Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCTCCTTCTC GCCGGTGG 18

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ser Pro Ser Arg Arg Trp
1 5

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Phe Val Leu Phe His Lys Ile Pro Leu Asp Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Trp Val Phe Ser Asn Ile Asp Asn His Gly Ile Leu Asn Leu Lys
1 5 10 15

Asp Asn Arg Asp His Leu Val Pro Ser Thr His Tyr Ile Tyr Glu
20 25 30

Glu Pro Glu Val Gln Ser Gly Glu Val Ser Tyr Pro Arg Ser His
35 40 45

Gly Phe Arg Glu Ile Met Leu Asn Pro Ile Ser Leu Pro Gly His
50 55 60

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